



- 1 -

SEQUENCE LISTING

<110> Lipton, Stuart A.
Okamoto, Shu-ichi

<120> Methods of Differentiating and
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> 66654-622

<140> US 09/876,187

<141> 2001-06-05

<150> US 60/209,539

<151> 2000-06-05

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2975

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (415)...(1935)

<400> 1

```
gaatttttctg caaggatcat atctaagtgc acttttttgcg gatacttcat ttctagacat 60
tgagtctcac tctaccccc aggctgaagt gcagtgggtg gatctcggtt cactgcaacc 120
tcgcctcca ggttcaagtg attctcgtac ctcagcctcc cgagtagctg ggattacagg 180
cgctgccac catgcctggc tgatatttat atttttagta gagatggagt ttcaccatgt 240
tggccaggct ggtctcgaac tctggacctc agatcttgta gaaaatttca gctgtagccc 300
ttggactaga agctgaaata acagaagctg tgtacgatgc attaggggtat tgaagaaaat 360
taacttttga attaaatatt tggaatataa ggaaataagg aaagttgact gaaa atg 417
Met
1
```

```
ggg cgg aag aaa ata caa atc aca cgc ata atg gat gaa agg aac cga 465
Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg
5 10 15
```

```
cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc tat 513
Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
20 25 30
```

```
gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc aac 561
Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn
35 40 45
```

```
agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa gtt 609
Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val
50 55 60 65
```

ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc aac	657
Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn	
70 75 80	
tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc gac	705
Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
85 90 95	
agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa	753
Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
100 105 110	
aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
115 120 125	
aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
130 135 140 145	
gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt	897
Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
150 155 160	
tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca	945
Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
165 170 175	
agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct	993
Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
180 185 190	
gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg ttg	1041
Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
195 200 205	
agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca gtg	1089
Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
210 215 220 225	
ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga gct	1137
Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
230 235 240	
act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc cct	1185
Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro	
245 250 255	
cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat ctt	1233
Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu	
260 265 270	
cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg	1281
Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
275 280 285	

gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct caa	1329
Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser Gln	
290 295 300 305	
gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca agc	1377
Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser	
310 315 320	
ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac aac	1425
Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn	
325 330 335	
act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc ttc	1473
Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe	
340 345 350	
aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag cag	1521
Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln	
355 360 365	
cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg cag	1569
His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln	
370 375 380 385	
tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc	1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser	
390 395 400	
atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg	1665
Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser	
405 410 415	
ggc ttc cag cag cag cag cag cag cag cag cag cag cag ccg ccg cca	1713
Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro	
420 425 430	
cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag gaa	1761
Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln Glu	
435 440 445	
atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc tat	1809
Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Tyr	
450 455 460 465	
gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca att	1857
Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile	
470 475 480	
gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct gta	1905
Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val	
485 490 495	
aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt	1955
Lys Arg Met Arg Met Asp Ala Trp Val Thr	
500 505	

ttgtactttt gtgttactgc agtgacctgc cctacatatc taaatcggta aataaggaca 2015

```

tgagttaa atatttat gtacatacat atatatatcc ctttacatat atatgtatgt 2075
gggtgtgagt gtgtgtgtat gtgtgggtgt gtgttacata cacagaatca ggcacttacc 2135
tgcaaaactcc ttgtaggtct gcagatgtgt gtcccatggc agacaaagca ccctgtaggc 2195
acagacaagt ctggcacttc cttggactac ttgtttcgta aagataacca gtttttgtag 2255
agaaacgtgt acccatatat aattctccca cactagcttg cagaaaccta gagggccccc 2315
tacttgtttt atttaactgt gcagtgtactg tagttactta agagaaaatg cttttagtaa 2375
cagagcagta gaaaagcagg aaccaagaaa gcaatactgt acataaaatg tcatttatat 2435
tttccaacct ggcattgggtg tctgttgcaa aggggtgcat gggaaagggc tgttgatatt 2495
aaaaacaaac aaaaacaaaa agccccacac ataactgttt tgcacgtgca aaaatgtatt 2555
gggtcaagaa gtgatcttta gctaataaag aaagagaata gaaaacacgc atgagatatt 2615
cagaaaatac tagcctagaa atatagagca ttaacaaagg aaaattaata tattaagtta 2675
taattggaat atgtcagaag tttcttttta cattcatatc ttaaaaatta aagaaactga 2735
ttttagctca tgtatatattt atatgaaaga aaacaccctt atgaattgat gactatatat 2795
aaaattatat tcactacttt tgaacacatt ctgctatgaa ttatttatat aagccaaagc 2855
tatatgttgt aacttttttt tagagaatag ctttatcttg gtttaactct ttagttttat 2915
ttaagaggg gaaaacaaaa atatcttgca agcagaacct tgaaaaaaa aaaggaattc 2975

```

<210> 2

<211> 507

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
 1          5          10          15
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20          25          30
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35          40          45
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50          55          60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65          70          75          80
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85          90          95
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
100          105          110
Glu Lys Tyr Lys Lys Ile Asn Glu Phe Asp Asn Met Met Arg Asn
115          120          125
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
130          135          140
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
145          150          155          160
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
165          170          175
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
180          185          190
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
195          200          205
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
210          215          220
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
225          230          235          240
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
245          250          255
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp

```

260	265	270
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu		
275	280	285
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser		
290	295	300
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro		
305	310	315
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr		
325	330	335
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly		
340	345	350
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln		
355	360	365
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly		
370	375	380
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile		
385	390	395
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro		
405	410	415
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro		
420	425	430
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln		
435	440	445
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser		
450	455	460
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro		
465	470	475
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser		
485	490	495
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr		
500	505	

<210> 3
 <211> 1671
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (443)...(1537)

<400> 3
 cggggggtcgc tatggaggag ccggagatgc agctcaaggg gaagaaagtc acggacaagt 60
 tcactgagag cgtctacgtc ctggccaacg agccatccgt ggccctgtac cggctgcagg 120
 agcatgtgcg tcgctccctc cccgagctgg cccagcaciaa ggagacatg cagcgttggg 180
 aggagcagag ccaggagacc atctacactg tggagtacgc ctgcagcgcc gtgaagaacc 240
 tgggtggacag cagcgtctac ttccgcagcg tggagggtct gctcaaacag gccatcagca 300
 tccgggacca tatgaatgcc agtgcccagg gccacagccc ggaggaacca ccccgccct 360
 cctcagctg atcctggaag agactcgggg ccccccagcc tccgccaacc cagacaaaga 420
 tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
 1 5 10
 atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
 Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
 15 20 25

ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag	568
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu	
30 35 40	
ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc	616
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala	
45 50 55	
agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag	664
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu	
60 65 70	
ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg	712
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg	
75 80 85 90	
agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct	760
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro	
95 100 105	
gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat	808
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp	
110 115 120	
ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc	856
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro	
125 130 135	
agc cca gat gtg gta tac ggg gcc tta ccg cca cca ggc tgt gac ccc	904
Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro	
140 145 150	
agt ggg ctt ggg gaa gca ctg ccc gcc cag agc cgc cca tct ccc ttc	952
Ser Gly Leu Gly Glu Ala Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe	
155 160 165 170	
cga cca gca gcc ccc aaa gcc ggg ccc cca ggc ctg gtg cac cct ctc	1000
Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu	
175 180 185	
ttc tca cca agc cac ctc acc agc aag aca cca ccc cca ctg tac ctg	1048
Phe Ser Pro Ser His Leu Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu	
190 195 200	
ccg acg gaa ggg cgg agg tca gac ctg cct ggt ggc ctg gct ggg ccc	1096
Pro Thr Glu Gly Arg Arg Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro	
205 210 215	
cga ggg gga cta aac acc tcc aga agc ctc tac agt ggc ctg cag aac	1144
Arg Gly Gly Leu Asn Thr Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn	
220 225 230	
ccc tgc tcc act gca act ccc gga ccc cca ctg ggg agc ttc ccc ttc	1192
Pro Cys Ser Thr Ala Thr Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe	
235 240 245 250	

ctc ccc gga ggc ccc cca gtg ggg gcc gaa gcc tgg gcg agg agg gtc 1240
 Leu Pro Gly Gly Pro Pro Val Gly Ala Glu Ala Trp Ala Arg Arg Val
 255 260 265

ccc caa ccc gcg gcg cct ccc cgc cga ccc ccc cag tca gca tca agt 1288
 Pro Gln Pro Ala Ala Pro Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser
 270 275 280

ctg agc gcc tct ctc cgg ccc ccg ggg gcc ccg gcg act ttc cta aga 1336
 Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg
 285 290 295

cct tcc cct atc cct tgc tcc tcg ccc ggt ccc tgg cag agc ctc tgc 1384
 Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys
 300 305 310

ggc ctg ggc ccg ccc tgc gcc ggc tgc cct tgg ccg acg gct ggc ccc 1432
 Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro
 315 320 325 330

ggt agg aga tca ccc ggt ggc acc agc cca gag cgc tcg cca ggt acg 1480
 Gly Arg Arg Ser Pro Gly Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr
 335 340 345

gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag 1528
 Ala Arg Ala Arg Gly Asp Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys
 350 355 360

acc caa cag tgacgcccc ctccgcggtg ggggcttggg ggtgggcggc 1577
 Thr Gln Gln
 365

tggactcaat ccaccctggg gggctccttt ccttcttctt atttgtgtgt atatccacaa 1637
 ataaaacgcg cgtggcgtcc gtggacacaaa aaaa 1671

<210> 4
 <211> 365
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn
 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
 85 90 95
 Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
 100 105 110
 Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro
 115 120 125

Arg	Leu	Tyr	Pro	Ala	Ala	Pro	Ala	Met	Pro	Ser	Pro	Asp	Val	Val	Tyr
130						135					140				
Gly	Ala	Leu	Pro	Pro	Pro	Gly	Cys	Asp	Pro	Ser	Gly	Leu	Gly	Glu	Ala
145					150				155						160
Leu	Pro	Ala	Gln	Ser	Arg	Pro	Ser	Pro	Phe	Arg	Pro	Ala	Ala	Pro	Lys
			165					170						175	
Ala	Gly	Pro	Pro	Gly	Leu	Val	His	Pro	Leu	Phe	Ser	Pro	Ser	His	Leu
		180						185					190		
Thr	Ser	Lys	Thr	Pro	Pro	Pro	Leu	Tyr	Leu	Pro	Thr	Glu	Gly	Arg	Arg
		195					200					205			
Ser	Asp	Leu	Pro	Gly	Gly	Leu	Ala	Gly	Pro	Arg	Gly	Gly	Leu	Asn	Thr
	210				215						220				
Ser	Arg	Ser	Leu	Tyr	Ser	Gly	Leu	Gln	Asn	Pro	Cys	Ser	Thr	Ala	Thr
225					230					235					240
Pro	Gly	Pro	Pro	Leu	Gly	Ser	Phe	Pro	Phe	Leu	Pro	Gly	Gly	Pro	Pro
			245					250						255	
Val	Gly	Ala	Glu	Ala	Trp	Ala	Arg	Arg	Val	Pro	Gln	Pro	Ala	Ala	Pro
		260						265					270		
Pro	Arg	Arg	Pro	Pro	Gln	Ser	Ala	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Arg
		275				280						285			
Pro	Pro	Gly	Ala	Pro	Ala	Thr	Phe	Leu	Arg	Pro	Ser	Pro	Ile	Pro	Cys
	290				295						300				
Ser	Ser	Pro	Gly	Pro	Trp	Gln	Ser	Leu	Cys	Gly	Leu	Gly	Pro	Pro	Cys
305					310					315					320
Ala	Gly	Cys	Pro	Trp	Pro	Thr	Ala	Gly	Pro	Gly	Arg	Arg	Ser	Pro	Gly
			325					330						335	
Gly	Thr	Ser	Pro	Glu	Arg	Ser	Pro	Gly	Thr	Ala	Arg	Ala	Arg	Gly	Asp
		340						345					350		
Pro	Thr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Lys	Thr	Gln	Gln			
		355				360						365			

<210> 5
 <211> 4077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (402)...(1820)

<400> 5
 gaattcccag ctctctgctc gctctgctcg cagtcacaga cacttgagca cacgcgtaca 60
 ccagacatc ttcgggctgc tattggattg actttgaagg ttctgtgtgg gtcgccgtgg 120
 ctgcatgttt gaatcagggtg gagaagcact tcaacgctgg acgaagtaaa gattattggt 180
 gttatttttt ttttctctct ctctctctct taagaaagga aaatatccca aggactaatc 240
 tgatcgggtc ttccttcac aggaacgaat gcaggaattt ggggaactgag ctgtgcaagt 300
 gctgaagaag gagatttggt tggaggaaac aggaaagaga aagaaaagga aggaaaaaat 360
 acataatttc agggacgaga gagagaagaa aaacggggac t atg ggg aga aaa aag 416
 Met Gly Arg Lys Lys
 1 5
 att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt 464
 Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
 10 15 20
 aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg 512

Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala	Tyr	Glu	Leu	Ser	Val		
			25					30					35				
ctg	tgt	gac	tgt	gag	att	gcg	ctg	atc	atc	ttc	aac	agc	acc	aac	aag	560	
Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	Asn	Ser	Thr	Asn	Lys		
		40					45					50					
ctg	ttc	cag	tat	gcc	agc	acc	gac	atg	gac	aaa	gtg	ctt	ctc	aag	tac	608	
Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys	Val	Leu	Leu	Lys	Tyr		
	55					60					65						
acg	gag	tac	aac	gag	ccg	cat	gag	agc	cgg	aca	aac	tca	gac	atc	gtg	656	
Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr	Asn	Ser	Asp	Ile	Val		
	70				75				80						85		
gag	acg	ttg	aga	aag	aag	ggc	ctt	aat	ggc	tgt	gac	agc	cca	gac	ccc	704	
Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys	Asp	Ser	Pro	Asp	Pro		
			90					95						100			
gat	gcg	gac	gat	tcc	gta	ggg	cac	agc	cct	gag	tct	gag	gac	aag	tac	752	
Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu	Ser	Glu	Asp	Lys	Tyr		
			105					110					115				
agg	aaa	att	aac	gaa	gat	att	gat	cta	atg	atc	agc	agg	caa	aga	ttg	800	
Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile	Ser	Arg	Gln	Arg	Leu		
		120					125					130					
tgt	gct	gtt	cca	cct	ccc	aac	ttc	gag	atg	cca	gtc	tcc	atc	cca	gtg	848	
Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro	Val	Ser	Ile	Pro	Val		
		135				140					145						
tcc	agc	cac	aac	agt	ttg	gtg	tac	agc	aac	cct	gtc	agc	tca	ctg	gga	896	
Ser	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro	Val	Ser	Ser	Leu	Gly		
	150				155				160						165		
aac	ccc	aac	cta	ttg	cca	ctg	gct	cac	cct	tct	ctg	cag	agg	aat	agt	944	
Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser	Leu	Gln	Arg	Asn	Ser		
			170						175					180			
atg	tct	cct	ggg	gta	aca	cat	cga	cct	cca	agt	gca	ggg	aac	aca	ggg	992	
Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser	Ala	Gly	Asn	Thr	Gly		
			185					190					195				
ggg	ctg	atg	ggg	gga	gac	ctc	acg	tct	ggg	gca	ggc	acc	agt	gca	ggg	1040	
Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala	Gly	Thr	Ser	Ala	Gly		
		200				205						210					
aac	ggg	tat	ggc	aat	ccc	cga	aac	tca	cca	ggg	ctg	ctg	gtc	tca	cct	1088	
Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly	Leu	Leu	Val	Ser	Pro		
		215				220					225						
ggg	aac	ttg	aac	aag	aat	atg	caa	gca	aaa	tct	cct	ccc	cca	atg	aat	1136	
Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser	Pro	Pro	Pro	Met	Asn		
	230				235				240						245		
tta	gga	atg	aat	aac	cgt	aaa	cca	gat	ctc	cga	gtt	ctt	att	cca	cca	1184	

Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu Ile Pro Pro	
250 255 260	
ggc agc aag aat acg atg cca tca gtg tct gag gat gtc gac ctg ctt	1232
Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu Asp Val Asp Leu Leu	
265 270 275	
ttg aat caa agg ata aat aac tcc cag tcg gct cag tca ttg gct acc	1280
Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr	
280 285 290	
cca gtg gtt tcc gta gca act cct act tta cca gga caa gga atg gga	1328
Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly	
295 300 305	
gga tat cca tca gcc att tca aca aca tat ggt acc gag tac tct ctg	1376
Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu	
310 315 320 325	
agt agt gca gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct	1424
Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala	
330 335 340	
ctt cac ctt ggt tca gta act ggc tgg caa cag caa cac cta cat aac	1472
Leu His Leu Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn	
345 350 355	
atg cca cca tct gcc ctc agt cag ttg gga gct tgc act agc act cat	1520
Met Pro Pro Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His	
360 365 370	
tta tct cag agt tca aat ctc tcc ctg cct tct act caa agc ctc aac	1568
Leu Ser Gln Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn	
375 380 385	
atc aag tca gaa cct gtt tct cct cct aga gac cgt acc acc acc cct	1616
Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro	
390 395 400 405	
tcg aga tac cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt	1664
Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val	
410 415 420	
gac agc ttg agc agc tgt agc agt tcg tac gac ggg agc gac cga gag	1712
Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu	
425 430 435	
gat cac cgg aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg	1760
Asp His Arg Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser	
440 445 450	
ccg gac gaa agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa	1808
Pro Asp Glu Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu	
455 460 465	
gga tgg gca aca tgatcagatt attacttact agtttttttt tttttcttgc	1860

Gly Trp Ala Thr
470

```

agtgtgtgtg tgtgctatac cttaatgggg aaggggggtc gatatgcatt atatgtgccg 1920
tgtgtggaaa aaaaaaaagt cagggtactct gttttgtaaa agtactttta aattgcctca 1980
gtgatacagt ataaagataa acagaaatgc tgagataagc ttagcacttg agttgtacaa 2040
cagaacactt gtacaaaata gattttaagg ctaacttctt ttcactgttg tgctcctttg 2100
caaaatgtat gttacaatag atagtgtcat gttgcaggtt caacgttatt tacatgtaaa 2160
tagacaaaag gaaacatttg ccaaaagcgg cagatcttta ctgaaagaga gagcagctgt 2220
tatgcaacat atagaaaaat gtatagatgc ttggacagac ccggtaatgg gtggccattg 2280
gtaaatgtta ggaacacacc aggtcacctg acatcccaag aatgctcaca aacctgcagg 2340
catatcattg gcgtatggca ctcatataaa aggatcagag accattaaaa gaggaccata 2400
cctattaaaa aaaaatgtgg agttggaggg ctaacatatt taattaaata aataaataaa 2460
tctgggtctg catctcttat taaataaaaa tataaaaaata tgtacattac attttgctta 2520
ttttcatata aaaggtaaga cagagtttgc aaagcatttg tggctttttg tagtttactt 2580
aagccaaaaat gtgttttttt ccccttgata gcttcgctaa tattttaaac agtcctgtaa 2640
aaaacccaaaa aggacttttt gtatagaaag cactacccta agccatgaag aactccatgc 2700
tttgctaacc aagataactg ttttctcttt gtagaagttt tgtttttgaa atgtgtattt 2760
ctaattatat aaaaattata gaactcttta aaaaaatctg tgaaattaac atgcttgtgt 2820
atagctttct aatatatata atattatggt aatagcagaa gttttgttat cttaatagcg 2880
ggaggggggt atatttctgc agttgcacat ttgagtaact attttcttct tgttttcttt 2940
tactctgctt acattttata agtttaagggt cagctgtcaa aaggataacc tgtgggggta 3000
gaacatatca cattgcaaca ccctaaattg tttttaatac attagcaatc tattgggtca 3060
actgacatcc attgtatata ctagtttctt tcatgctatt tttattttgt tttttgcatt 3120
tttatcaaat gcagggcccc tttctgatct caccatttca ccatgcatct tggaattcag 3180
taagtgcata tccctaacttg cccatattct aaatcatctg gttgggtttc agcctagaat 3240
ttgatacgtt ttttagaaat atgcccagaa tagaaaagct atgttggggc acatgtcctg 3300
caaatatggc ctagaaaaca agtgatatgg aatttacttg gtgaataagt tataaattcc 3360
cacagaagaa aaatgtgaaa gactgggtgc tagacaagaa ggaagcaggt aaagggatag 3420
ttgctttgtc atccgttttt aattatttta actgaccctt gacaatcttg tcagcaatat 3480
aggactgttg aacaatcccg gtgtgtcagg accccc aaat gtcacttctg cataaagcat 3540
gtatgtcatc tattttttct tcaataaaga gatttaatag ccatttcaag aaatcccata 3600
aagaacctct ctatgtccct ttttttaatt taaaaaaatg actcttgtct aatattcgtc 3660
tataagggat taattttcag accctttaat aagtgaagtgc cataagaaag tcaatatata 3720
ttgtttaaaa gatatttcag tctaggaaag attttccttc tcttggaatg tgaagatctg 3780
tcgattcatc tccaatcata tgcattgaca tacacagcaa agaagatata ggcagtaata 3840
tcaacactgc tatatcatgt gtaggacatt tcttatccat tttttctctt ttacttgcatt 3900
agttgctatg tgtttctcat tgtaaaaggc tgccgctggg tggcagaagc caagagacct 3960
tattaactag gctatatatt tcttaacttg atctgaaatc cacaattaga ccacaatgca 4020
cctttgggtg tatccataaa ggatgctagc ctgccttgta ctaatgtttt atatatt 4077

```

<210> 6
<211> 473
<212> PRT
<213> Homo sapiens

```

<400> 6
Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
 1           5           10           15
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20           25           30
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35           40           45
Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50           55           60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65           70           75           80

```

Asn	Ser	Asp	Ile	Val	Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys	
				85					90					95		
Asp	Ser	Pro	Asp	Pro	Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu	
			100					105					110			
Ser	Glu	Asp	Lys	Tyr	Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile	
		115					120					125				
Ser	Arg	Gln	Arg	Leu	Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro	
	130						135				140					
Val	Ser	Ile	Pro	Val	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro		
145					150				155					160		
Val	Ser	Ser	Leu	Gly	Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser	
			165					170						175		
Leu	Gln	Arg	Asn	Ser	Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser	
			180					185					190			
Ala	Gly	Asn	Thr	Gly	Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala	
		195					200					205				
Gly	Thr	Ser	Ala	Gly	Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly	
	210					215					220					
Leu	Leu	Val	Ser	Pro	Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser	
225					230					235					240	
Pro	Pro	Pro	Met	Asn	Leu	Gly	Met	Asn	Asn	Arg	Lys	Pro	Asp	Leu	Arg	
			245					250						255		
Val	Leu	Ile	Pro	Pro	Gly	Ser	Lys	Asn	Thr	Met	Pro	Ser	Val	Ser	Glu	
			260					265					270			
Asp	Val	Asp	Leu	Leu	Leu	Asn	Gln	Arg	Ile	Asn	Asn	Ser	Gln	Ser	Ala	
		275					280					285				
Gln	Ser	Leu	Ala	Thr	Pro	Val	Val	Ser	Val	Ala	Thr	Pro	Thr	Leu	Pro	
	290					295					300					
Gly	Gln	Gly	Met	Gly	Gly	Tyr	Pro	Ser	Ala	Ile	Ser	Thr	Thr	Tyr	Gly	
305					310					315					320	
Thr	Glu	Tyr	Ser	Leu	Ser	Ser	Ala	Asp	Leu	Ser	Ser	Leu	Ser	Gly	Phe	
			325					330						335		
Asn	Thr	Ala	Ser	Ala	Leu	His	Leu	Gly	Ser	Val	Thr	Gly	Trp	Gln	Gln	
			340					345					350			
Gln	His	Leu	His	Asn	Met	Pro	Pro	Ser	Ala	Leu	Ser	Gln	Leu	Gly	Ala	
		355					360					365				
Cys	Thr	Ser	Thr	His	Leu	Ser	Gln	Ser	Ser	Asn	Leu	Ser	Leu	Pro	Ser	
	370					375					380					
Thr	Gln	Ser	Leu	Asn	Ile	Lys	Ser	Glu	Pro	Val	Ser	Pro	Pro	Arg	Asp	
385					390					395					400	
Arg	Thr	Thr	Thr	Pro	Ser	Arg	Tyr	Pro	Gln	His	Thr	Arg	His	Glu	Ala	
			405					410						415		
Gly	Arg	Ser	Pro	Val	Asp	Ser	Leu	Ser	Ser	Cys	Ser	Ser	Ser	Tyr	Asp	
			420					425					430			
Gly	Ser	Asp	Arg	Glu	Asp	His	Arg	Asn	Glu	Phe	His	Ser	Pro	Ile	Gly	
		435					440					445				
Leu	Thr	Arg	Pro	Ser	Pro	Asp	Glu	Arg	Glu	Ser	Pro	Ser	Val	Lys	Arg	
	450					455					460					
Met	Arg	Leu	Ser	Glu	Gly	Trp	Ala	Thr								
465					470											

<210> 7

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (196)...(1761)

<400> 7

```

caggggagag ggctacccgc tctttgccgt gacaacaccg ttccccagc cgggctggag 60
gctgtgcaga aggtatcctg cagaccatga actgagcact gttcccagac cgttcagag 120
cacagtgtaa ggtgtgccga gacccaccac ccagcgagcc cctccccctcc gtagcactga 180
ggacccccgg agaag atg ggg agg aaa aag att cag atc cag cga atc acc 231
      Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr
        1             5                     10

gac gag cgg aac cga cag gtg act ttc acc aag cgg aag ttt ggc ctg 279
Asp Glu Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu
      15             20                     25

atg aag aag gcg tat gag ctg agc gtg cta tgt gac tgc gag atc gca 327
Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala
      30             35                     40

ctc atc atc ttc aac cac tcc aac aag ctg ttc cag tac gcc agc acc 375
Leu Ile Ile Phe Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr
      45             50                     55                     60

gac atg gac aag gtg ctg ctc aag tac acg gag tac aat gag cca cac 423
Asp Met Asp Lys Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His
      65             70                     75

gag agc cgc acc aac gcc gac atc atc gag acc ctg agg aag aag ggc 471
Glu Ser Arg Thr Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly
      80             85                     90

ttc aat ggc tgc gac agc ccc gag ccc gac ggg gag gac tgc ctg gaa 519
Phe Asn Gly Cys Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu
      95             100                    105

cag agc ccc ctg ctg gag gac aag tac cga cgc gcc agc gag gag ctc 567
Gln Ser Pro Leu Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu
     110             115                    120

gac ggg ctc ttc cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt 615
Asp Gly Leu Phe Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe
    125             130                    135                    140

gcc atg cct gtc acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc 663
Ala Met Pro Val Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe
     145             150                    155

agc aat ccc agc ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc 711
Ser Asn Pro Ser Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser
     160             165                    170

ctc acg gac ccg cgg ctc ctg tcc ccc cag cag cca gca cta cag agg 759
Leu Thr Asp Pro Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg
     175             180                    185

aac agt gtg tct cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc 807

```

Asn Ser Val Ser Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala	
190 195 200	
atg ctg ggg ggt gac ctg aac agt gct aac gga gcc tgc ccc agc cct	855
Met Leu Gly Gly Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro	
205 210 215 220	
gtt ggg aat ggc tac gtc agt gct cgg gct tcc cct ggc ctc ctc cct	903
Val Gly Asn Gly Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro	
225 230 235	
gtg gcc aat ggc aac agc cta aac aag gtc atc cct gcc aag tct ccg	951
Val Ala Asn Gly Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro	
240 245 250	
ccc cca cct acc cac agc acc cag ctt gga gcc ccc agc cgc aag ccc	999
Pro Pro Pro Thr His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro	
255 260 265	
gac ctg cga gtc atc act tcc cag gca gga aag ggg tta atg cat cac	1047
Asp Leu Arg Val Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His	
270 275 280	
ttg act gag gac cat tta gat ctg aac aat gcc cag cgc ctt ggg gtc	1095
Leu Thr Glu Asp His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val	
285 290 295 300	
tcc cag tct act cat tcg ctc acc acc cca gtg gtt tct gtg gca acg	1143
Ser Gln Ser Thr His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr	
305 310 315	
ccg agt tta ctc agc cag ggc ctc ccc ttc tct tcc atg ccc act gcc	1191
Pro Ser Leu Leu Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala	
320 325 330	
tac aac aca gat tac cag ttg acc agt gca gag ctc tcc tcc tta cca	1239
Tyr Asn Thr Asp Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro	
335 340 345	
gcc ttt agt tca cct ggg ggg ctg tcg cta ggc aat gtc act gcc tgg	1287
Ala Phe Ser Ser Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp	
350 355 360	
caa cag cca cag cag ccc cag cag ccg cag cag cca cag cct cca cag	1335
Gln Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln	
365 370 375 380	
cag cag cca ccg cag cca cag cag cca cag cca cag cag cct cag cag	1383
Gln Gln Pro Pro Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln	
385 390 395	
ccg caa cag cca cct cag caa cag tcc cac ctg gtc cct gta tct ctc	1431
Pro Gln Gln Pro Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu	
400 405 410	
agc aac ctc atc ccg ggc agc ccc ctg ccc cac gtg ggt gct gcc ctc	1479
Ser Asn Leu Ile Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu	

415	420	425	
aca gtc acc acc cac ccc cac atc agc atc aag tca gaa ccg gtg tcc			1527
Thr Val Thr Thr His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser			
430	435	440	
cca agc cgt gag cgc agc cct gcg cct ccc cct cca gct gtg ttc cca			1575
Pro Ser Arg Glu Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro			
445	450	455	460
gct gcc cgc cct gag cct ggc gat ggt ctc agc agc cca gcc ggg gga			1623
Ala Ala Arg Pro Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly			
465	470	475	
tcc tat gag acg gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc			1671
Ser Tyr Glu Thr Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro			
480	485	490	
aca ctg ggc ctg ctg cgc cca gcc cca gag cct gag gct gag ggc tca			1719
Thr Leu Gly Leu Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser			
495	500	505	
gct gtg aag agg atg cgg ctt gat acc tgg aca tta aag tga			1761
Ala Val Lys Arg Met Arg Leu Asp Thr Trp Thr Leu Lys *			
510	515	520	
cgattccac tcccctctc tcagcctccc tgatgaagag ttgacaatct caccgcccgc			1821
ccttcctcgc cccgggctcc tcccgctcga cccccacttc ctttcttggtg cttegtgtcc			1881
tgttgacggt tacatttgtg tataattatt atattatt			1919

<210> 8

<211> 521

<212> PRT

<213> Homo sapiens

<400> 8

Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr Asp Glu Arg Asn	
1 5 10 15	
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys	
85 90 95	
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu	
100 105 110	
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe	
115 120 125	
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val	
130 135 140	
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser	
145 150 155 160	

Gly	Ser	Leu	Val	Thr	Pro	Ser	Leu	Val	Thr	Ser	Ser	Leu	Thr	Asp	Pro		
				165					170					175			
Arg	Leu	Leu	Ser	Pro	Gln	Gln	Pro	Ala	Leu	Gln	Arg	Asn	Ser	Val	Ser		
			180					185						190			
Pro	Gly	Leu	Pro	Gln	Arg	Pro	Ala	Ser	Ala	Gly	Ala	Met	Leu	Gly	Gly		
		195					200					205					
Asp	Leu	Asn	Ser	Ala	Asn	Gly	Ala	Cys	Pro	Ser	Pro	Val	Gly	Asn	Gly		
	210					215					220						
Tyr	Val	Ser	Ala	Arg	Ala	Ser	Pro	Gly	Leu	Leu	Pro	Val	Ala	Asn	Gly		
225					230					235					240		
Asn	Ser	Leu	Asn	Lys	Val	Ile	Pro	Ala	Lys	Ser	Pro	Pro	Pro	Pro	Thr		
				245					250						255		
His	Ser	Thr	Gln	Leu	Gly	Ala	Pro	Ser	Arg	Lys	Pro	Asp	Leu	Arg	Val		
			260					265						270			
Ile	Thr	Ser	Gln	Ala	Gly	Lys	Gly	Leu	Met	His	His	Leu	Thr	Glu	Asp		
		275					280					285					
His	Leu	Asp	Leu	Asn	Asn	Ala	Gln	Arg	Leu	Gly	Val	Ser	Gln	Ser	Thr		
	290					295					300						
His	Ser	Leu	Thr	Thr	Pro	Val	Val	Ser	Val	Ala	Thr	Pro	Ser	Leu	Leu		
305					310					315					320		
Ser	Gln	Gly	Leu	Pro	Phe	Ser	Ser	Met	Pro	Thr	Ala	Tyr	Asn	Thr	Asp		
				325					330						335		
Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Leu	Ser	Ser	Leu	Pro	Ala	Phe	Ser	Ser		
			340					345					350				
Pro	Gly	Gly	Leu	Ser	Leu	Gly	Asn	Val	Thr	Ala	Trp	Gln	Gln	Pro	Gln		
		355					360					365					
Gln	Pro	Gln	Gln	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Gln	Gln	Gln	Pro	Pro		
		370				375					380						
Gln	Pro	Gln	Gln	Pro	Gln	Pro	Gln	Gln	Pro	Gln	Gln	Pro	Gln	Gln	Pro		
385					390					395					400		
Pro	Gln	Gln	Gln	Ser	His	Leu	Val	Pro	Val	Ser	Leu	Ser	Asn	Leu	Ile		
				405					410					415			
Pro	Gly	Ser	Pro	Leu	Pro	His	Val	Gly	Ala	Ala	Leu	Thr	Val	Thr	Thr		
			420					425					430				
His	Pro	His	Ile	Ser	Ile	Lys	Ser	Glu	Pro	Val	Ser	Pro	Ser	Arg	Glu		
	435					440						445					
Arg	Ser	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Val	Phe	Pro	Ala	Ala	Arg	Pro		
	450					455					460						
Glu	Pro	Gly	Asp	Gly	Leu	Ser	Ser	Pro	Ala	Gly	Gly	Ser	Tyr	Glu	Thr		
465					470					475					480		
Gly	Asp	Arg	Asp	Asp	Gly	Arg	Gly	Asp	Phe	Gly	Pro	Thr	Leu	Gly	Leu		
				485					490					495			
Leu	Arg	Pro	Ala	Pro	Glu	Pro	Glu	Ala	Glu	Gly	Ser	Ala	Val	Lys	Arg		
		500						505					510				
Met	Arg	Leu	Asp	Thr	Trp	Thr	Leu	Lys									
		515					520										

<210> 9

<211> 8

<212> PRT

<213> Homo sapiens

<400> 9

Ser Glu Glu Glu Glu Leu Glu Leu

1 5

<210> 10
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 10
 Thr Glu Asp His Leu Asp Leu
 1 5

<210> 11
 <211> 8
 <212> PRT
 <213> Homo sapiens

<400> 11
 Ser Glu Asp Val Asp Leu Leu Leu
 1 5

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 12
 tgggctataa atagccgc

18

<210> 13
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 9, 10, 11, 12, 13, 14, 15, 16, 17
 <223> Xaa = Any Amino Acid

<400> 13
 Pro Thr Lys Ser Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Arg Lys Pro Asp Leu Arg Val Val
 20 25

<210> 14
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 14

Thr Pro Val Val Ser Val Thr Thr Pro Ser Leu Pro Pro Gln Gly Leu
 1 5 10 15
 Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn Thr Asp Tyr Ser Leu Thr
 20 25 30
 Ser Ala Asp Leu Ser Ala Leu
 35

<210> 15
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 15
 Ile Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg
 1 5 10

<210> 16
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 16
 Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Tyr Asp
 1 5 10 15
 Gly Ser Asp Arg Glu Asp
 20

<210> 17
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 9, 10, 11, 12, 13, 14
 <223> Xaa = Any Amino Acid

<400> 17
 Gln Ala Lys Ser Pro Pro Pro Met Xaa Xaa Xaa Xaa Xaa Xaa Arg Lys
 1 5 10 15
 Pro Asp Leu Arg Val Leu
 20

<210> 18
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 18
 Thr Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met
 1 5 10 15
 Gly Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser
 20 25 30

Leu Ser Ser Ala Asp Leu Ser Ser Leu
35 40

<210> 19
<211> 14
<212> PRT
<213> Homo sapiens

<400> 19
Leu Ser Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg
1 5 10

<210> 20
<211> 22
<212> PRT
<213> Homo sapiens

<400> 20
Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Gly
1 5 10 15
Asp Ser Asp Arg Glu Asp
20

<210> 21
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
<223> Xaa = Any Amino Acid

<400> 21
Pro Ala Lys Ser Pro Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Arg Lys Pro Asp Leu Arg Val Ile
20 25

<210> 22
<211> 39
<212> PRT
<213> Homo sapiens

<400> 22
Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu Ser Gln Gly Leu
1 5 10 15
Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp Tyr Gln Leu Pro
20 25 30
Ser Ala Glu Leu Ser Ser Leu
35

<210> 23
<211> 14
<212> PRT
<213> Homo sapiens

<400> 23
Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu Arg
1 5 10

<210> 24
<211> 12
<212> PRT
<213> Homo sapiens

<400> 24
Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val Glu
1 5 10

<210> 25
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 25
ytaatataata ttar